REMARKS/ARGUMENTS

Reconsideration of the above-identified application is respectfully requested in view of the amendments to the claims and the following remarks.

Claims 4, 7, 10, 33 and 34 have been cancelled.

Claims 1 and 6 have been amended.

Claims 1-3, 5-6, 8-9, and 11-32 remain in the case.

No revision of inventorship is necessary in the present application.

Support for the Amendment

Claims 1 and 6 have been amended to include the language suggested by Examiner Robinson, in the May 11, 2005 Office Action. No other changes to the claims have been made.

The specification has been amended to correct the informalities noted by Examiner Robinson, in the May 11, 2005 Office Action. These changes include changes to the Brief Description to correct the format of the sequence notation, changes to the Brief Description to reflect the currently revised drawings, and to correct page 102, line 34. Changes to other portions of the specification have also been made to correct the format of the sequence notation. Additional changes have been made to correct spelling informalities. No new material has been added.

The figures 4.16-4.18, 8.43, and 8.44 have been revised to eliminated color and color references, using asterisks, letters, and outline boxes in place of color. No new material has been added.

Invention Summary

Thermal hysteresis proteins (THPs) also known as antifreeze proteins are known to lower the non-equilibrium freezing point of water without lowering the melting point (equilibrium freezing point). The present invention details relative recrystallization inhibition behavior of thermal hystersis proteins. In particular, extremely dilute solutions of THPs have been shown to inhibit the recrystallization of fine-grained ice samples in a concentration-dependent manner. The high sensitivity of RI to the presence of THPs led Applicants to the present invention, as recited in the amended claims, which is a quantitative assay of THP activity using the recrystallization inhibition behavior. The extent of recrystallization in a fine-grained ice sample is quantified by estimating mean largest cross-sectional area for ice grains in the sample, thus providing the basis for a numerical assessment of RI. A number of different assay characteristics is addressed and described in the specification, including specificity of the RI assay with respect to THP, ice grain size homogeneity within RI ice samples, RI assay sensitivities, applications of the assay, and assay automation.

As defined in currently amended claim 1, the invention particularly defines a relative recrystallization inhibition analysis method for determining the presence, relative concentration, and activity of THPs. A test solution made of a proteinaceous composition in a solvent is flash frozen; the temperature of the frozen solution is raised to an appropriate annealing temperature that allows for a partial melt, while limiting heterogeneity in ice grain sizes within the solution. The frozen solution is maintained at the annealing temperature for a length of time sufficient to allow for ice recrystallization. Changes in ice crystal grain size are monitored over time; and the presence of functional THPs (while reducing the effect of non-specific proteins) in the solution is determined by measuring ice crystal grain sizes relative to a control solution.

Conclusion

In view of the above remarks and amendment to the claims, to the figures, and to the specification, Applicants believe they have overcome the objections noted. Applicants request reconsideration of this application and allowance of pending claims 1-3, 5-6, 8-9, and 11-32.

I hereby certify that this correspondence is being deposited with the United States Postal Service as first class mail in an envelope addressed to:

Mail Stop _____
Commissioner for Patents
P.O. Box 1450
Alexandria, VA 22313-1450

On 8/9/05 (Date of Deposit)

Mark Levy, Reg. No. 29,188 8/9/05 (Date)

Respectfully submitted,
MARK LEVY & ASSOCIATES, PLLC

By: Mark Levy
Registration No. 29,188
Attorney for Applicant
Press Building - Suite 902
19 Chenango Street
Binghamton, New York 13901
Phone: (607) 722-6600

Attachment: Appendix with amended and annotated drawing Figures.

Amendments to the Drawings:

The attached sheet of drawings includes changes to Fig. 2.6c. This sheet replaces the original sheet including Fig. 2.6c. This figure now shows proper spelling of "residue" in the heading beginning with "A". The color highlighting has removed from Figures 4.16, 4.17, 4.18, 8.43, and 8.44, and replaced with arrows, asterisks, and boxes. See annotated Figures 4.16, 4.17, 4.18, 8.43, and 8.44.

Attachment: Replacement Sheets for figures: 2.6c, 4.16, 4.17, 4.18, 8.43, and 8.44. Annotated sheets for 2.6c, 4.16, 4.17, 4.18, 8.43, and 8.44.

A. Mature Tm 13.17 amino acid residue

1 LTEAQIEKLN KISKKCQNES GVSQEIITKA RNGDWEDDPK LKRQVFCVAR

61 NAGLATESGE VVVDVLREKV RKVTDNDEET EKIINKCAVK RDTVEETVFN

121 TFKCVMKNKP KFSPVD

B. Summary of the composition analysis for the mature Tm 13.17 sequence:

Residue	Number	Mole Percent
A = Ala	6	5.172
B = Asx	0	0.000
C = Cys	4	3.448
D = Asp	8	6.897
E = Glu	13	11.207
F = Phe	4	3.448
G = Gly	4	3.448
H = His	0	0.000
I = Ile	6	5.172
K =Lys	16	13.793
L = Leu	5	4.310
M = Met	1	0.862
N = Asn	8	6.897
P = Pro	3	2.586
Q = Gln	4	3.448
R = Arg	6	5.172
S = Ser	5	4.310
T = Thr	8	6.897
V =Val	14	12.069
W = Trp	1	0.862
Y = Tyr	0	0.000
Z = Glx	0	0.000

Molecular weight = 13171.96; Residues = 116; Average Residue Weight = 113.551

Charge = 1; Isoelectric point = 7.74.

FIG 2.6c

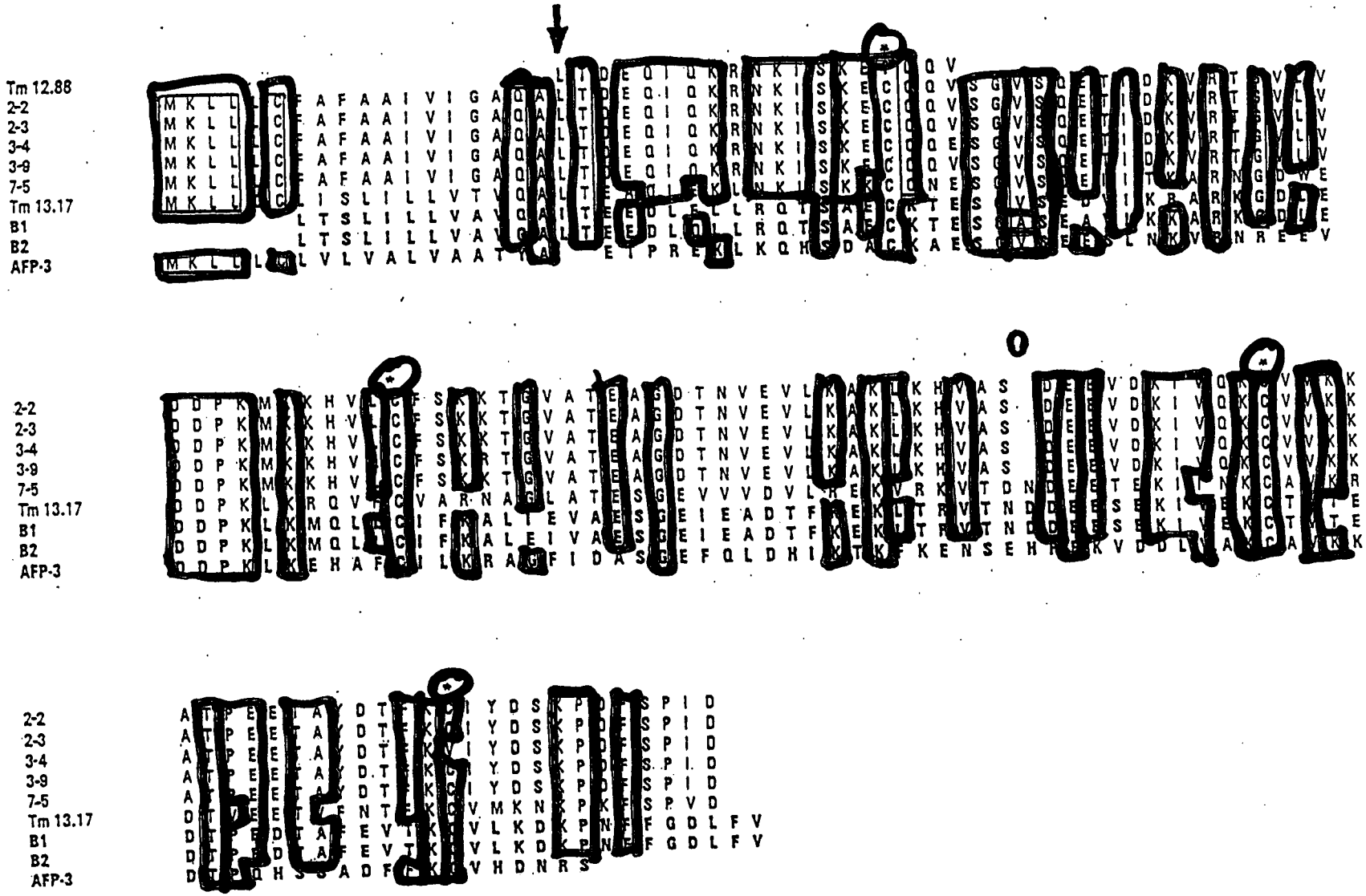

Fig. 4.16

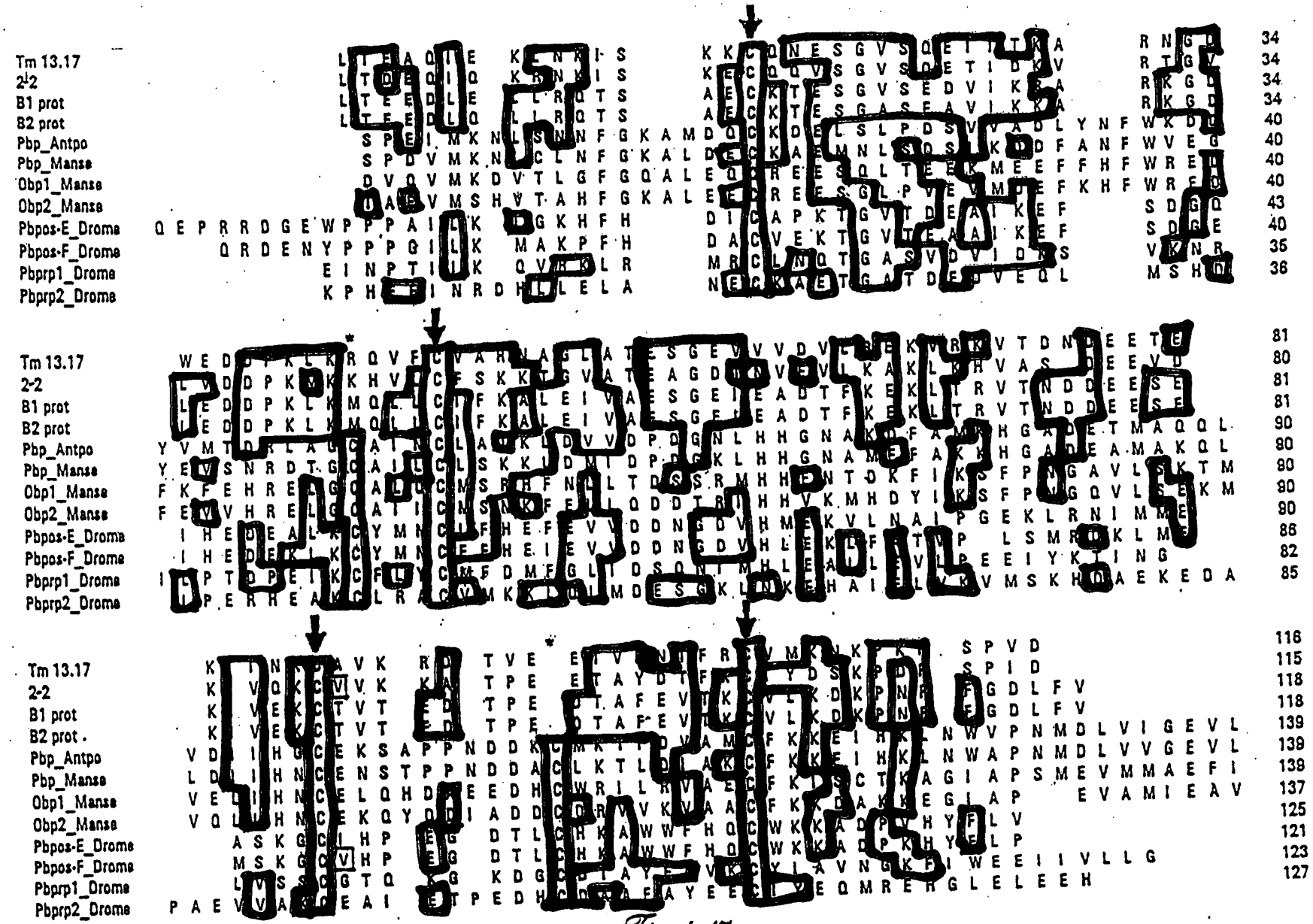
Tm 13.17
2-2
B1 prot
B2 prot
Pbp_Antpo
Pbp_Manse
Obp1_Manse
Obp2_Manse
Pbpos-E_Drome
Pbpos-F_Drome
Pbprp1_Drome
Pbprp2_Drome
34
34
34
34
40
40
40
40
43
40
35
36
81
80
81
81
90
90
90
90
90
86
82
85
116
115
118
118
139
139
139
137
125
121
123
127

Fig. 4.17

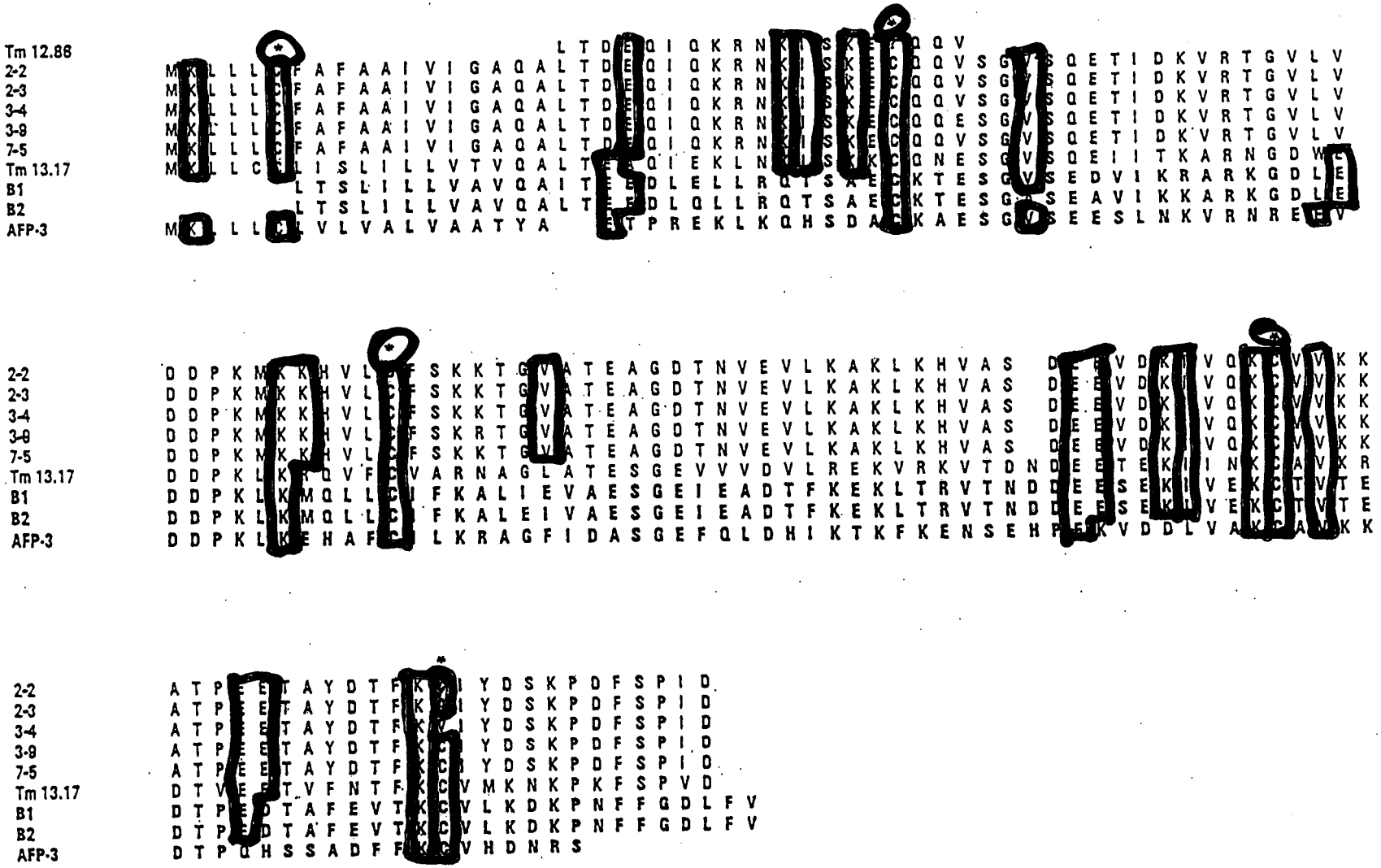

Fig. 4.18

DNA sequence of Tm 13.17 cDNA clone

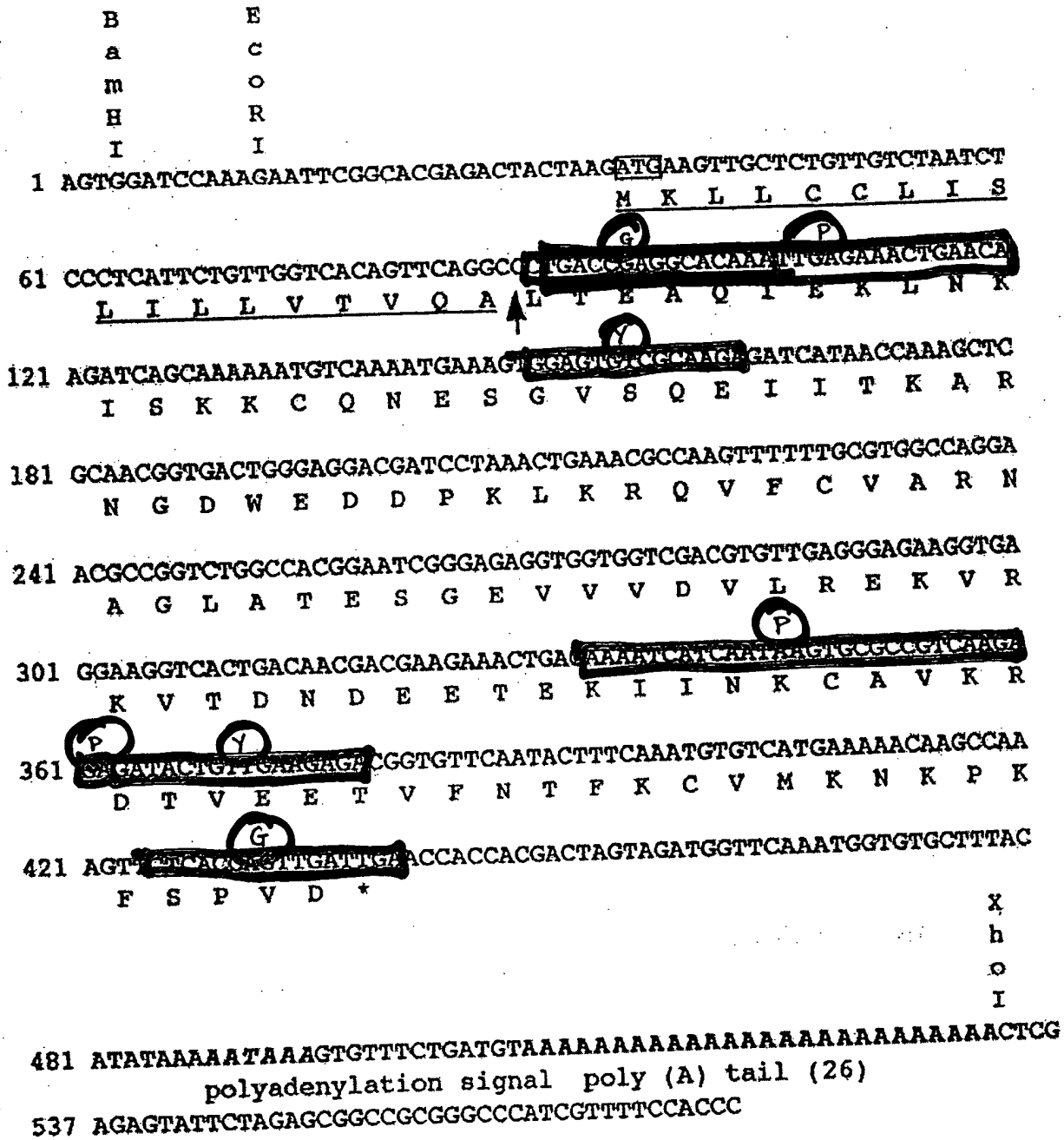

Fig. 8.43

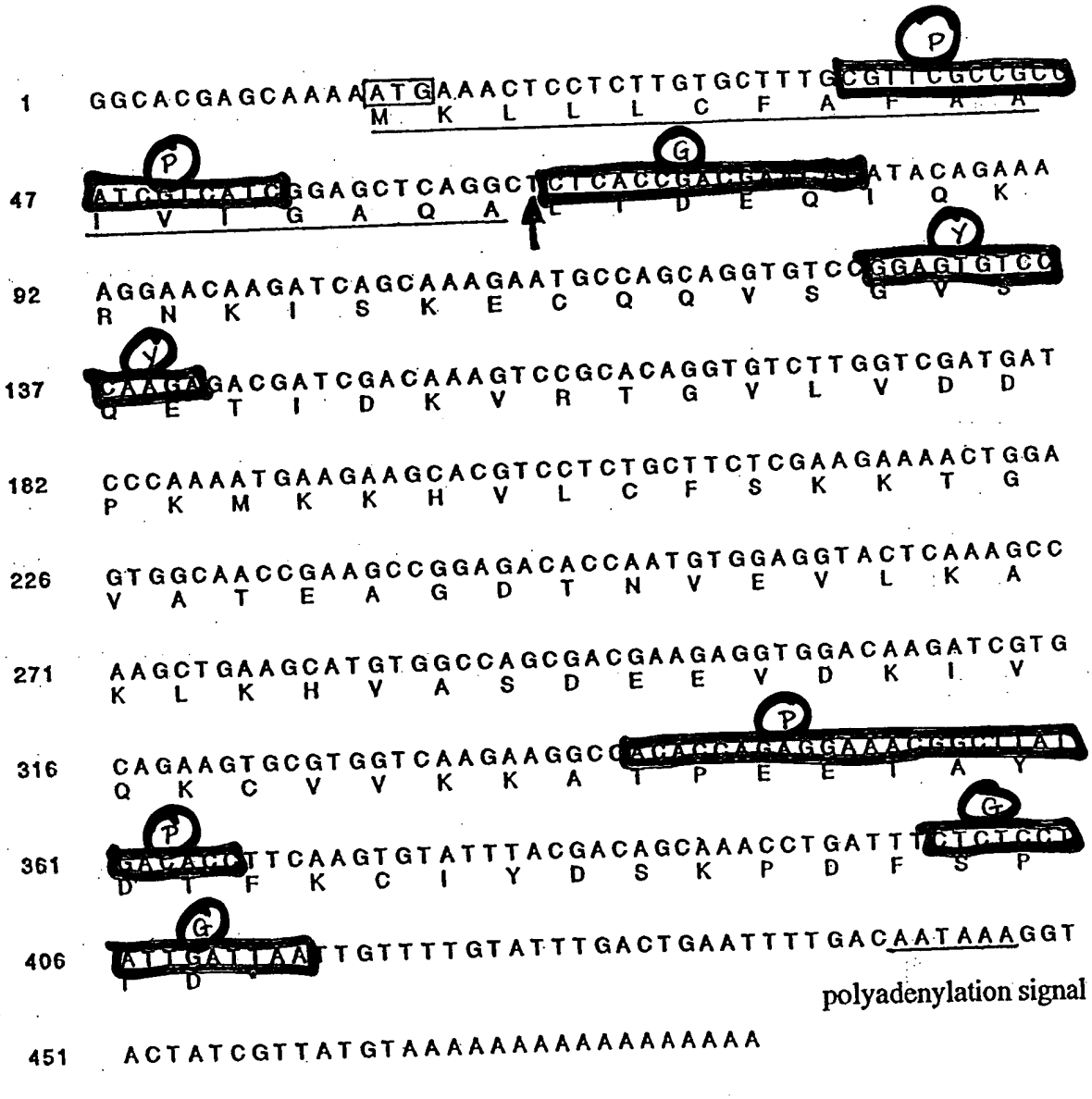
1 GGCACGAGCAAAA ATG AAACTCCTCTTGTGCTTTG
M K L L L C F A
47 GGAGCTCAGGCT
I V I G A Q A
92 AGGAACAAGATCAGCAAAGAATGCCAGCAGGTGTCC
R N K I S K E C Q Q V S
137 GACGATCGACAAAGTCCGCACAGGTGTCTTGGTCGATGAT
Q E T I D K V R T G V L V D D
182 CCCAAAATGAAGAAGCACGTCCTCTGCTTCTCGAAGAAAACTGGA
P K M K K H V L C F S K K T G
226 GTGGCAACCGAAGCCGGAGACACCAATGTGGAGGTACTCAAAGCC
V A T E A G D T N V E V L K A
271 AAGCTGAAGCATGTGGCCAGCGACGAAGAGGTGGACAAGATCGTG
K L K H V A S D E E V D K I V
316 CAGAAGTGCGTGGTCAAGAAGGCC
Q K C V V K K A
361 TTCAAGTGTATTTACGACAGCAAACCTGATTT
F K C I Y D S K P D F
406 TTGTTTTGTATTTGACTGAATTTTGAC AATAAA GGT
polyadenylation signal
451 ACTATCGTTATGTAAAAAAAAAAAAAAAA
poly (A) tail

Fig. 8.44